

Genetic Analysis of Alaskan Coho Salmon

Evidence for population structure at small geographic scales

Introduction

Coho salmon (Figure 1) are one of five species of Pacific salmon found in North America. In Alaska, coho salmon are distributed from the Dixon Entrance in Southeast Alaska, north to Point Hope in the Chukchi Sea, and are the fourth most abundant species of Pacific salmon. Alaskan coho salmon are found in a variety of freshwater systems, such as large tributaries of the Yukon River and recently de-glaciated coastal streams in Glacier Bay. However, many coho salmon populations occupy small headwater streams with limited spawning and juvenile rearing habitat. These populations are small in size and tend to spawn late in the year (early fall to mid winter) as compared to other Pacific salmon.

Alaska represents half of the North American range for coho salmon. However, information for coho in Alaska is limited. Little is known about their genetic diversity and population structure. It is critical that we obtain this information in order to provide the foundation on which to develop and evaluate conservation and management plans.

Methods

In 1997, the U.S. Fish and Wildlife Service Alaska Region Conservation Genetics Laboratory (CGL) initiated a genetic study to examine the population structure of Alaskan coho salmon. The objective of the study was to estimate and evaluate the degree and spatial distribution of genetic diversity in Alaskan coho salmon.

Fin clips were collected from 50-100 coho salmon from each of 32 putative populations across Alaska (Figures 2 and 3). These samples were genotyped with nine microsatellite DNA markers



Figure 1. Male coho salmon from the Kenai River drainage.

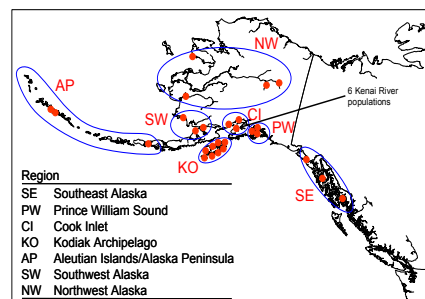


Figure 2. Map of Alaskan coho salmon populations sampled.

to estimate population structure within and among seven geographic regions. Intensive sampling in the Kenai River and on the Kodiak Archipelago also allowed for detailed intra-regional analysis.

Population Structure

The degree of population structure in coho salmon was determined by estimating F_{ST} , which is the fraction of the total genetic diversity from all populations due to variation



Figure 3. Collecting fin tissue from a coho salmon. After sampling, fish are returned to the stream to spawn.

between populations (Figure 4). Obstinably, F_{ST} is a measure of genetic distinctiveness and can be no less than zero (no population structure) and no greater than 1 (completely isolated populations).

Isolation By Distance

The spatial distribution of genetic diversity was also evaluated by testing for genetic isolation by distance (IBD) over all populations and within the Kodiak Archipelago and Kenai

River. IBD exists if the genetic distance between populations increases (is correlated) with geographic distance (Figure 5).

Results

Our results provide insight into the degree and distribution of genetic diversity in Alaskan coho salmon and have important conservation implications:

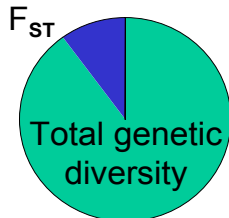


Figure 4. The blue wedge represents an F_{ST} of approximately 0.10 or 10%.

First, the results show that the degree of population structure is high for all 32 populations (Figure 6), and is as large or larger than that reported for other species of Pacific salmon in Alaska. Coho salmon population structure occurs on a relatively fine geographic scale.

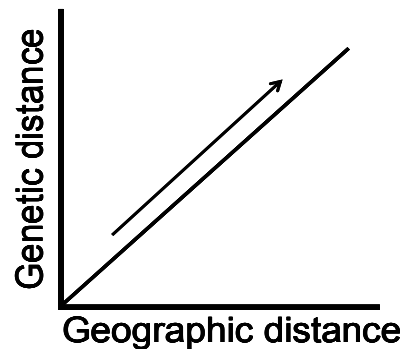


Figure 5. The theoretical relationship between genetic and geographic distance under isolation by distance (IBD).

Second, our results show that genetic and geographic distances are not correlated at broad geographic scales. Within

intensively sampled regions, genetic and geographic distances are correlated for the Kenai River populations, but not for the Kodiak Archipelago populations. Isolation by distance occurs only at the finest geographic scale and suggests that coho salmon in Alaska are comprised of many small and genetically discrete populations. These results provide an important genetic foundation to guide future studies to precisely define conservation boundaries for Alaskan coho salmon.

Any management or conservation actions affecting coho salmon in Alaska must recognize that their populations are clearly structured at small geographic scales. Activities or conditions that cause declines in abundance are more likely to have strong negative impacts for coho salmon than for species in which genetic variation is distributed over a broader geographic scale (e.g., chum salmon). Coho populations are small, isolated, and contain relatively large amounts of genetic variation. Therefore, they are more susceptible to extirpation and less likely to be augmented or “rescued” by other nearby populations. Every coho population lost represents the loss of significant amounts of genetic variability.

Current coho projects

We are presently conducting three additional coho genetic studies using microsatellites to estimate population contributions in mixed stock aggregations. We are examining Kenai River coho salmon to determine the population composition of juveniles emigrating from the river system each spring. This information will help biologists evaluate and develop management strategies to protect important life history traits such as the annual timing of adult return. We are also examining in more detail the population structure of coho salmon in the Kuskokwim and Yukon Rivers. This information can be used to develop population composition estimates for adult coho salmon harvested in mixed-stock fisheries. All of these projects will facilitate evaluation of current management strategies and allow for the conservation of healthy coho salmon populations in Alaska. Furthermore, evaluating the natural mechanisms that create and maintain genetic diversity in the relatively pristine and unaltered salmon populations in Alaska may facilitate conservation efforts along the West Coast of the U.S. where anthropogenic factors have obscured natural patterns.

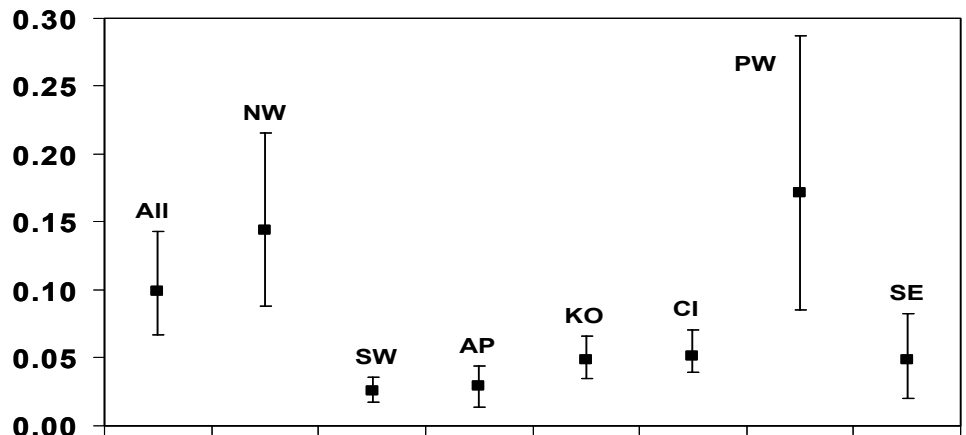


Figure 6. Estimates of the degree of population structure (F_{ST}) for all 32 coho salmon population samples and for population samples from each region. The vertical lines indicate 95% confidence intervals for each estimate.

For additional details, see: Olsen JB, Miller SJ, Spearman WJ and Wenburg JK (2003) Patterns of intra- and inter-population genetic diversity in Alaskan coho salmon: Implications for conservation. *Conservation Genetics*, 4, 557-569.

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